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Metabolic tracing unravels pathways of fungal and bacterial amino sugar formation in soil

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Abstract

© 2018 British Society of Soil Science The present study aimed to reveal the steps in the formation of fungal and bacterial amino sugars (AS) from glucose. Glucose labelled uniformly and position-specifically at C-1, C-2, C-4 and C-6 was applied to an agricultural soil. Fungal and bacterial pathways of AS formation were reconstructed by a new approach: 13C recovery from individual C positions of glucose in AS by IC-O-IRMS. Only 0.75% of 13C from initially applied glucose was incorporated into AS within 10 days and followed the order: glucosamine > galactosamine > muramic acid. Relative incorporation of 13C (% of AS-C) had the largest values for bacterial muramic acid and the smallest for fungal galactosamine. This reflects faster turnover of bacterial than fungal cell walls. A maximum of 55% ± 19% of the 13C incorporated in glucosamine was derived from intact, untransformed glucose. The smallest recovery was observed for C-1 and C-4. Recovery of C-1 even decreased from day 3 to day 10, reflecting the metabolization by the pentose phosphate pathway. To be incorporated into AS, metabolites resulting from either the pentose phosphate pathway or glycolysis needed to be reconstructed to glucose by the reversible pathways of gluconeogenesis. The direct formation of AS (e.g. intact recovery of the glucose precursor), as well as amino sugar formation from recycled metabolites allocated to the hexose pool by back flux, occurred in parallel. Bacterial muramic acid showed the most variation in the recovery of individual C positions during 10 days, which reflects its intensive transformation by glycolysis, pentose phosphate pathway and gluconeogenesis. It is explained by the lower metabolic activity of fungi than bacteria at steady-state conditions. The present approach enabled us to analyse the biochemical pathways in bacteria and fungi, which will considerably improve our understanding of the formation and stabilization of microbially derived SOM compounds. Highlights: Fungal and bacterial pathways of the formation of amino sugars from glucose are reconstructed Intact use of glucose is distinguished from recycling by a metabolic tracing approach Half of the precursor (glucose) is metabolized prior to incorporation into amino sugars Intracellular recycling plays a crucial role in microbial SOM formation.

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